

#### SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: OHTOMO, Toshihiko SATO, Koh TSUCHIYA, Masayuki
- (ii) TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN MEDULLOBLASTOMA CELLS
- (iii) NUMBER OF SEQUENCES: 132
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Foley & Lardner
  - (B) STREET: 3000 K Street, N.W., Suite 500
  - (C) CITY: Washington
  - (D) STATE: D.C.
  - (E) COUNTRY: USA
  - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/646,265
  - (B) FILING DATE: 09-SEP-1996
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: WO PCT/JP94/01763
  - (B) FILING DATE: 19-OCT-1994
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: JP 5-291078
  - (B) FILING DATE: 19-NOV-1993
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: WEGNER, Harold C.
  - (B) REGISTRATION NUMBER: 25,258
  - (C) REFERENCE/DOCKET NUMBER: 53466/184
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (202)672-5300
    - (B) TELEFAX: (202)672-5399
    - (C) TELEX: 904136
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 40 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG	40
(2) INFORMATION FOR SEQ ID NO:2:	
(i) SEQUENCE CHARACTERISTICS:	•
(A) LENGTH: 39 base pairs	•
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
ACTAGTCGAC ATGGAGWCAG ACACACTCCT GYTATGGGT	39
(2) INFORMATION FOR SEQ ID NO:3:	•
/; ) CROHENCE CHADACTEDICTICS.	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 40 base pairs</li></ul>	
(B) TYPE: nucleic acid	•
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(b) TOPOLOGI: Timear	
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	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	•
ACTAGTCGAC ATGAGTGTGC TCACTCAGGT CCTGGSGTTG	40
(2) INFORMATION FOR SEQ ID NO:4:	•
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 43 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG

(2) INFORMATION FOR SEQ ID NO:5:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 40 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
ACTAGTCGAC ATGGATTTWC AGGTGCAGAT TWTCAGCTTC	40
(2) INFORMATION FOR SEQ ID NO:6:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 37 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  ACTAGTCGAC ATGAGGTKCY YTGYTSAGYT YCTGRGG	37
(2) INFORMATION FOR SEQ ID NO:7:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 41 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	
ACTAGTCGAC ATGGGCWTCA AGATGGAGTC ACAKWYYCWG G	41
(2) INFORMATION FOR SEQ ID NO:8:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 41 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	

(B)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:		
ACTAGTCGAC ATGTGGGGAY CTKTTTYCMM TTTTTCAATT G	;	41
(2) INFORMATION FOR SEQ ID NO:9:		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 35 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>		
	,	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:		
ACTAGTCGAC ATGGTRTCCW CASCTCAGTT CCTTG		35
(2) INFORMATION FOR SEQ ID NO:10:	•	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 37 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:		
ACTAGTCGAC ATGTATATAT GTTTGTTGTC TATTTCT		37
(2) INFORMATION FOR SEQ ID NO:11:		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 38 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>		
•		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:		
ACTAGTOGAC ATGGAAGCCC CAGCTCAGCT TCTCTTCC		38
		20
(2) INFORMATION FOR SEQ ID NO:12:		
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 27 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single		



(xi) SEQUENCE DESCRIPTION:	SEQ ID NO:12:			
GGATCCCGGG TGGATGGTGG GAAGATG				27
(2) INFORMATION FOR SEQ ID NO:	13•			
(2) Infoldation for BEQ ID No.		•		
(i) SEQUENCE CHARACTERIST:  (A) LENGTH: 37 base p  (B) TYPE: nucleic acc  (C) STRANDEDNESS: sin  (D) TOPOLOGY: linear	pairs id		·	
	•			
(xi) SEQUENCE DESCRIPTION:	SEQ ID NO:13:			
ACTAGTCGAC ATGAAATGCA GCTGGGTCA	AT STTCTTC	•		37
(2) INFORMATION FOR SEQ ID NO:	L4:			
(i) SEQUENCE CHARACTERIST	cs:			
(A) LENGTH: 36 base p				
(B) TYPE: nucleic act				
(C) STRANDEDNESS: sir	ngle		•	
(D) TOPOLOGY: linear			٠	
		-		
(xi) SEQUENCE DESCRIPTION:	SEQ ID NO:14:			
ACTAGTCGAC ATGGGATGGA GCTRTATCA	AT SYTCTT		*	36
(2) INFORMATION FOR SEQ ID NO:				
(i) SEQUENCE CHARACTERIST	cs:			
(A) LENGTH: 37 base p	pairs			
(B) TYPE: nucleic aci				
(C) STRANDEDNESS: sir	ngle	•		
(D) TOPOLOGY: linear				
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			•	
•				
	•			
(xi) SEQUENCE DESCRIPTION:	SEO ID NO:15:			
, . = , <u>~</u>				

ACTAGTCGAC ATGAAGWTGT GGTTAAACTG GGTTTTT



	(2)	INFORMATION FOR SEQ ID NO:16:	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 35 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
		(b) ToroLogi: Timedi	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
		(XI) BEQUENCE DESCRIPTION. SEQ ID NO.10.	
	ACT	AGTCGAC ATGRACTTTG GGYTCAGCTT GRTTT	35
		MOTORIO MICHAELIO COLLONOCII CALIII	
	(2)	INFORMATION FOR SEQ ID NO:17:	
	(-)	Internation for Bug ID Novi,	
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 40 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
		(b) Totobodi. Tindai	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
		(1.1) 01201101 012011 012 10 10111	
	ACT	AGTCGAC ATGGACTCCA GGCTCAATTT AGTTTTCCTT	40
•			
	(2)	INFORMATION FOR SEQ ID NO:18:	
			•
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 37 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
		(5) 20102011 22::001	
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
		(AI) DECOMED BEDONII IION. BEQ ID NO. 10.	
	ACTA	AGTCGAC ATGGCTGTCY TRGSGCTRCT CTTCTGC	37
	(2)	INFORMATION FOR SEQ ID NO:19:	
	` '		
		(i) SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 36 base pairs	
		(B) TYPE: nucleic acid	
	-	(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:		
ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT		36
(2) INFORMATION FOR SEQ ID NO:20:		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 33 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>		
	•	
	•	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:		
ACTAGTCGAC ATGAGAGTGC TGATTCTTTT GTG		33
(2) INFORMATION FOR SEQ ID NO:21:		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 40 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:		
ACTAGTCGAC ATGGMTTGGG TGTGGAMCTT GCTATTCCTG		40
(2) INFORMATION FOR SEQ ID NO:22:		
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 37 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:		
ACTAGTCGAC ATGGGCAGAC TTACATTCTC ATTCCTG		37
(2) INFORMATION FOR SEQ ID NO:23:		
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 38 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>		-

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:		
ACTAGTCGAC ATGGATTTTG GGCTGATTTT TTTTATTG	•	38
(2) INFORMATION FOR SEQ ID NO:24:		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 37 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:		
ACTAGTCGAC ATGATGGTGT TAAGTCTTCT GTACCTG		37
(2) INFORMATION FOR SEQ ID NO:25:		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 28 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:		
GGATCCCGGG CCAGTGGATA GACAGATG		. 28
(2) INFORMATION FOR SEQ ID NO:26:		•
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 382 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>		

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..381

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

				GTC Val						48
				GTG Val						96
				GTC Val					AAT Asn	144
				TGG Trp 55						192
				GCA Ala						240
				TCT Ser						288
			-	TTG Leu						336
				GGT Gly						381
C.										382

#### (2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 127 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Glu Ser His Ile Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser 1 5 10 15

Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser 20 25 30

Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn 35 40 45

Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro 50 55 60

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Lys 65	Pro	Leu	Ìle	Tyr	Ser 70	Ala	Ser	Tyr	Arg	Tyr 75	Ser	Gly	Val	Pro	Asp 80		
Arg	Phe	Thr	Gly	Ser 85	Gly	Ser	Gly	Thr	Asp 90	Phe	Thr	Leu	Thr	Ile 95	Thr		
Asn	Val	Gln	Ser 100	Glu	Asp	Leu	Ala	Asp 105	Tyr	Phe	Cys	Gln	Gln 110	Tyr	Asn		
Ser	Tyr	Pro 115	Arg	Ala	Phe	Gly	Gly 120	Gly	Thr	ГÀЗ	Leu	Glu 125	Ile	Lys			
(2)	INFO	ORMA'	rion	FOR	SEQ	ID I	NO: 28	3:									
	(i)	(1 (1	A) LI B) T: C) S:	engti Ype : Trani	nuci DEDNI	CTER D9 ba leic ESS: line	ase p acio sino	pair:	5				·				
	(ix)	( 2		AME/I		CDS	108										
	(ix)	( 2		AME/I		mat_ 14	_	cide		_							
	(xi)	SEÇ	QUENC	CE DI	ESCRI	PTIC	on: s	EQ I	D NO	28:	:						
	AAA Lys																48
	AAT Asn																96
	GGG Gly																144
	GAC Asp 50																192
	TGG Trp																240
	AAG Lys															-	_288





GCC Ala									336
 TAC Tyr	 	 							384
 ACC Thr 130	 	 Val		G			٠		409

#### (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 136 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly
1 5 10 15

Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys 20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile 35 40 45

Lys Asp Thr Tyr Ile His Trp Ala Lys Gln Arg Pro Glu Gln Gly Leu 50 60

Glu Trp Ile Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp 65 70 75 80

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn 85 90 95

Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val 100 105 110

Tyr Tyr Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Ser Val Thr Val Ser Ser 130 135

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
GATAAGCTTC CACCATGGGC TTCAAGATGG AGTC	34
(2) INFORMATION FOR SEQ ID NO:31:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 34 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
GGCGGATCCA CTCACGTTTG ATTTCCAGTT TGGT	34
(2) INFORMATION FOR SEQ ID NO:32:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 43 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
GATAAGCTTC CACCATGAAA TGCAGCTGGG TCATGTTCTT CCT	43
(2) INFORMATION FOR SEQ ID NO:33:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 34 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
GGCGGATCCA CTCACCTGAG GAGACGGTGA CTGA	_ 34
(2) INFORMATION FOR SEQ ID NO:34:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCCTATCGGT ACAGTGGTGT GCCAAGCAGA TTCAGCGG

(D) TOPOLOGY: linear		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	•	
CAGACAGTGG TTCAAAGT		18
(2) INFORMATION FOR SEQ ID NO:35:		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 26 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:		
GAATTCGGAT CCACTCACGT TTGATT		26
(2) INFORMATION FOR SEQ ID NO:36:		
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 44 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>		
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:		
AGTCAGAATG TGGGTACTAA TGTAGCCTGG TACCAGCAGA AGCC		44
(2) INFORMATION FOR SEQ ID NO:37:		
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 38 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	Ye .	

(2) INFORMATION FOR SEQ 1D NO.30.	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 47 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
GCTACCTACT ACTGCCAGCA ATATAACAGC TATCCTCGGG CGTTCGG	47
(2) INFORMATION FOR SEQ ID NO:39:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 44 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(D) TOPOLOGI: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
ACATTAGTAC CCACATTCTG ACTGGCCTTA CAGGTGATGG TCAC	44
(2) INFORMATION FOR SEQ ID NO:40:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 47 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG	47
(2) INFORMATION FOR SEQ ID NO:41:	
(i) SEQUENCE CHARACTERISTICS:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 44 base pairs	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 44 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
(A) LENGTH: 44 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	-
(A) LENGTH: 44 base pairs (B) TYPE: nucleic acid	-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGA	TAGC	TGT	TATA	TTGC	TG G	CAGT	AGTA	G GT	AGCG	ATGT	CCT	С				4	4
(2)	INF	ORMA	TION	FOR	SEQ	ID	NO: 4	2:									
	(i	(	QUEN A) L B) T C) S D) T	ENGT YPE: TRAN	H: 3 nuc DEDN	79 b leic ESS:	ase aci dou	pair d	s S			-					
٠			è													×	
	(ix	. (	ATUR A) N B) L	AME/			378					,					
	(ix	(.	ATUR A) N B) L	AME/				tide									
	(xi	) SE	QUEN	CE D	ESCR:	IPTI	ON:	SEO :	ID N	0:42	:						
ATG	GGA	•	_					_				ACA	GCT	ACA	GGT	4	8
	Gly																
	CAC His															9	6
	GTG Val 15															. 14	4
	ACT Thr															19	2
	CTG Leu															24	0
	AGC Ser															28	8
	CAG Gln															33	6
	CCT Pro 95													· · · ·		37	8.
С																37	9

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- (2) INFORMATION FOR SEQ ID NO:43:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 126 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

31

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

- (2) INFORMATION FOR SEQ ID NO:44:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 31 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGTACCGACT ACACCTTCAC CATCAGCAGC C

- (2) INFORMATION FOR SEQ ID NO:45:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 31 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single



## (D) TOPOLOGY: linear

																-	
	(xi)	) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0:45	:						
GGT	GAAGO	GTG '	TAGT	CGGT	AC C	GCTA	CCGC	T A									3:
(2)	INFO	DRMA'	TION	FOR	SEO	ID	NO:4	6:									
(-,					_												
	(1)		_			CTER 79 b			g								
5		-	-			leic		-	_								
		(	c) s	TRAN	DEDN:	ESS:	dou	ble									
		(1	D) T	OPOL	OGY:	lin	ear										
	(ix)		ATUR														
			•	•		CDS											
		, ,		0111	2011.		3,0										
	(ix)		ATUR														
						mat_ 58.	_	tide									
		(1	ט נכ	JCAI.	ION:	50.	. 3 / 0										
	(xi)	SEÇ	QUEN	CE DI	ESCR	IPTIC	: NC	SEQ :	ID NO	<b>D:4</b> 6	:						
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TCC	TTG	GTA	GCA	ACA	GCT	ACA	GGT		48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Ser	Leu	Val	Ala	Thr	Ala	Thr	Gly		
-19				-15					-10					<b>-</b> 5		•	
GTĊ	CAC	TCC	GAC	ATC	CAG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC		96
	His																
			1				5					10					
AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATC	ACC	TGT	AAG	GCC	AGT	CAG	AAT	GTG		144
Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asn	Val		
	15					20				-	25						•
GGT	ACT	AAT	GTA	GCC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	AAG	GCT	CCA	ÄAG		192
	Thr																
30					35					40					45		
CTG	CTG	ATC	TAC	TCG	GCA	TCC	тат	CGG	TAC	AGT	сст	GTG	CCA	AGC	AGA		240
	Leu																
				50				_	55					60			
ጥጥር	AGC	сст	AGC	ССТ	AGT	CGT	ACC	GAC	ጥልሮ	ACC	ጥጥር	ACC	АТС	AGC	AGC		288
	Ser																200
		-	65	•				70	-				75	•			

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90 336

()

TAT	CCT	CGG	GCG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA
Tyr	Pro	Arg	Ala	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys
	95					100					105		

378

С

379

- (2) INFORMATION FOR SEQ ID NO:47:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 126 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 20

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg

Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser 70 65

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

- (2) INFORMATION FOR SEQ ID NO:48:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 29 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GCTACCTACT TCTGCCAGCA ATATAACAG

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

		(1	B) T	YPE: TRAN	H: 25 nuc DEDNI	leic ESS:	acio sino	d							•	
		١														
				~~ ~		* D.M.T.		SEO :		2 - 40	_			-		
	(x1	) SE	SORM	CE D	ESCR.	IPTI	. : NC	SEQ .	או מז	J:49	•			. •		
TGC	rggc	AGA A	AGTA	GGTA(	GC G	ATGT	CCTC									29
(2)	INF	ORMA	rion	FOR	SEQ	ID I	NO: 50	0:								
	(i	(1	A) LI B) T C) S	engti YPE : Irani		79 ba leic ESS:	ase p acid doub	pairs 1	5							
	(ix	•	A) NA	AME/I	KEY: ION:		378			÷ .						
	•	-	A) NA B) LO	AME/I	KEY: ION:	58.	378		ID NO	o: 50:						
														 		4.0
		TGG Trp														48
		TCC Ser	Asp			Met	Thr		Ser	Pro	Ser	Ser	Leu			96
		GGT Gly														144
		AAT Asn														192
		ATC Ile														240
		GGT Gly														288

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 379

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

# (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 379 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

## (ix) FEATURE:

(A) NAME/KEY: CDS



(B) LOCATION: 1..378

# (ix) FEATURE:

(A) NAME/KEY: mat\_peptide
(B) LOCATION: 58..378

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

			AGC Ser							48
,			GAC Asp 1						-	96
			GAC Asp							144
			GTA Val		 	 				192
			TAC Tyr							240
			AGC Ser 65							288
			GAG Glu							336
			GCG Ala							378
	c į									379

# (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10 -5



Val	His	Ser	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	
Ser	Val 15	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Сув	Lys	Ala 25	Ser	Gln	Asn	Val	
Gly 30	Thr	Asn	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	
Leu	Leu	Ile	Tyr	Ser 50	Ala	Ser	Tyr	Arg	Tyr 55	Ser	Gly	Val	Pro	Ser 60	Arg	
Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Tyr	Thr	Phe	Thr	Ile 75	Ser	Ser	
Leu	Gln	Pro 80	Glu	Asp	Ile	Ala	Thr 85	Tyr	Phe	Cya	Gln	Gln 90	Tyr	Asn	Ser	
Tyr	Pro 95	Arg	Ala	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys			
(2)	INFO	DRMAT	noi	FOR	SEQ	ID N	10:54	1:								
		( E	A) LE B) TY C) ST O) TO	PE: PANE POLC	nucl EDNE OGY:	leic ESS: line	acio sino ear	d gle								
3	(xi)	SEÇ	QUENC	E DE	SCRI	PTIC	ON: S	SEQ I	D NO	):54:	•					
TGAG	CAGAG	TG 1	CCGI	CACC	T GI	PAAGO	CCA					÷				25
(2)	INFO	RMAI	NOI	FOR	SEQ	ID N	Ю:55	5:			•					
	(i)	(E	QUENCA) LE B) TY C) ST	NGTE PE: RAND	nucl	bas Leic ESS:	se pa acio sino	airs 1								
		·							•							
	(xi)	SEÇ	OUENC	E DE	SCRI	PTIC	on: S	SEQ I	D NC	):55:	:					
TTAC	CAGGI	GA C	CGGAC	CACTO	T GI	CACC	CCAC									29
(2)	INFO	RMAI	NOI	FOR	SEQ	ID N	10:56	5:								

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 379 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double

#### (D) TOPOLOGY: linear

ı	Ίi	v	١.	FEATURE	٠
ı	_	^	,	PERTURE	•

(A) NAME/KEY: CDS
(B) LOCATION: 1..378

#### (ix) FEATURE:

(A) NAME/KEY: mat\_peptide
(B) LOCATION: 58..378

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

		AGC Ser								4.8	3
	_	GAC Asp						•		96	5
	 	GAC Asp		 _						144	1
		GTA Val								192	2
		TAC Tyr								240	)
		AGC Ser 65								288	3
		GAG Glu								336	5
		GCG Ala	-							378	3
С										379	€

# (2) INFORMATION FOR SEQ ID NO:57:

# (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(z

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57: Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10 -5 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

# (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 379 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

# (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

## (ix) FEATURE:

15

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..378

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

20

	TGG Trp	Ser							48
Val				Thr					96
AGC Ser	GGT Glv		 	 	 	 	 		144



GGT	ACT	AAT	GTA	GCC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	AAG	GCT	CCA	AAG		192
Gly	Thr	Asn	Val	Ala	Trp	Tyr	Gln	Gln.	Lys	Pro	Gly	Lys	Ala	Pro	Lys		
30					35					40					45		
		ATC															240
Leu	Leu	Ile.	Tyr	Ser	Ala	Ser	Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Ser	Arg	•	
				50					55					60			
		GGT															288
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	`	
			65					70					75				
		CCA															336
Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Phe	Cys	Gln		Tyr	Asn	Ser		
		80					85					90					
		CGG							•								378
Tyr		Arg	Ala	Phe	Gly		Gly	Thr	Lys	Val		Ile	Lys				
	95			,		100					105						
									· .								
С																	379

### (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105



(2)	) INFORMATION FOR SEQ ID NO:60:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 26 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
GĄC	CTTCACCT TGACCATCAG CAGCCT	26
(2)	) INFORMATION FOR SEQ ID NO:61:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 26 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
	GCTGATGG TCAAGGTGAA GTCGGT	26
(2)	) INFORMATION FOR SEQ ID NO:62:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 379 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(in) EDATUDE.	
	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1378	
	<pre>(ix) FEATURE:    (A) NAME/KEY: mat_peptide    (B) LOCATION: 58378</pre>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	•
	G GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT CGly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	48
	C CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC L His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10	96

AGC	GTG	GGT	GAC	AGA	GTG	TCC	GTC	ACC	TGT	AAG	GCC	AGT	CAG	AAT	GTG	144
Ser	Val 15	Gly	Asp	Arg	Val	Ser 20	Val	Thr	Cys	ГÀЗ	Ala 25	Ser	Gln	Asn	Val	
							CAG Gln									192
							TAT Tyr									240
							ACC Thr									288
							ACC Thr 85									336
							GGG Gly									378
С			-													3.79

(2) INFORMATION FOR SEQ ID NO:63:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

#### (ii) MOLECULE TYPE: protein

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 . 5 10

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser 80 85 90 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

#### (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..378

# (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 58..378

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

					GCA Ala			48
					AGC Ser			96
			Ile		GCC Ala 25			144
					GGA Gly			192
					GGT Gly			240
					TTG Leu			288
					CAG Gln			336
 -					GAA Glu 105			378

B

- (2) INFORMATION FOR SEQ ID NO:65:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 126 amino acids
      - (B) TYPE: amino acid
      - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

29

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

- (2) INFORMATION FOR SEQ ID NO:66:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 29 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGACAGAGTC CAAAGCCGCT GATCTACTC

- (2) INFORMATION FOR SEQ ID NO:67:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 29 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

										,				•	
ATC	AGCG	GCT	TTGG	ACTO	TG T	CCTG	GCTI	•		,					29
(2)	INF	'ORMA	TION	FOF	SEQ	ID	NO: 6	8:	ŕ						
0.0	(1	(	A) L B) T C) S	ENGT YPE: TRAN	HARA H: 3 nuc DEDN	79 b leic ESS:	ase aci dou	pair d	<b>s</b>						
	(ix	(	•	AME/	KEY: ION:								•		
	(ix	) FE	ATUR A) N	E: AME/	KEY:	mat <sub>.</sub>	_pep			,					
<i>y</i>	(xi				ESCR:				ID N	0:68	:			-	
					ATC Ile										48
					CAG Gln										96
					GTG Val										144
					TGG Trp 35									•	192
					GCA Ala										240
					AGC Ser										288

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser

85

80

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

378

С

379

#### (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

#### (ii) MOLECULE TYPE: protein

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
1 5 10

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GAGGACATCG CTGACTACTT CTGCCA



(2) INFORMATION FOR SEQ ID NO:71:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 26 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
AAGTAGTCAG CGATGTCCTC TGGCTG	26
(2) INFORMATION FOR SEQ ID NO:72:	20
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 379 base pairs	
(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
(D) TOPOLOGY: linear	
(ix) FEATURE: (A) NAME/KEY: CDS	
(B) LOCATION: 1378	
<pre>(ix) FEATURE:     (A) NAME/KEY: mat peptide</pre>	
(B) LOCATION: 58.378	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	144
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	192
30 35 40 45	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	240
50 55 60	

TTC AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser

70

65

288

						CAA Gln 90			336
						ATC Ile			378
С									379

#### (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 379 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

#### (ix) FEATURE:

(A) NAME/KEY: CDS



#### (B) LOCATION: 1..378

# (ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 58..378

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

		AGC Ser						 		48
		GAC Asp 1						 		96
		GAC Asp								144
		GTA Val							•	192
		TAC Tyr								240
		AGC Ser 65								288
		GAG Glu								336
		GCG Ala								378
С				*					•	379

# (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

(h)

Val	His	Ser	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala	
Ser	Val 15	Gly	Asp	Arg	Val	Ser 20	Val	Thr	Cys	Lys	Ala 25	Ser	Gln	Asn	Val	
Gly 30		Asn	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45	
Leu	Leu	Ile	Tyr	Ser 50	Ala	Ser	Tyr	Arg	<b>Tyr</b> 55	Ser	Gly	Val	Pro	Ser 60	-	
Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70		Thr	Leu	Thr	Ile 75	Ser	Ser	
Leu	Gln	Pro 80	Glu	Asp	Ile	Ala	Asp 85	Tyr	Phe	Cys	Gln	Gln 90	Tyr	Asn	Ser	
Tyr	Pro 95	Arg	Ala	Phe	Gly	Gln 100	Gly	Thr	Lys	Val	Glu 105	Ile	Lys			
(2)	INF	ORMA:	rion	FOR	SEQ	ID 1	NO:76	<b>5:</b>			•	-			•	
	(i	SEC	QUENC	E CE	IARAC	TTER	ISTI	as:			•					
	( -		A) LE						5							
4		-	3) T)						•						•	
			C) SI O) TO					ore								
		-	•						•							
	(ix)		ATURE		rev.	CDE									•	
		-	A) N <i>F</i> B) LC	•			378									
	( i sr )	. E-E-7	ATURE													
	(17)		A) NE		EY:	mat_	_pept	ide	•							
	•	( E	B) LC	CAT	ON:	58	.378				-					
	(xi)	SEÇ	QUENC	CE DE	ESCRI	PTIC	on: s	SEQ 1	D NO	76:	:					
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TCC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	48
Met -19	Gly	Trp	Ser	Cys -15	Ile	Ile	Leu	Ser	Leu -10	Val	Ala	Thr	Ala	Thr	-	
-19				-15	,				-10					- 3	•	
			GAC													96
var	птэ	ser	Asp 1	116	GIII	Mec	5	GIII	Ser	PLU	ser	10	Leu	Jer	ALG	•
AGC	GTG	GGT	GAC	AGA	GTG	TCC	GTC	ACC	TGT	AAG	GCC	AGT	CAG	AAT	GTG	144
Ser		Gly	Asp	Arg	Val		Val	Thr	Cys	Lys	_	Ser	Gln	Asn	Val	
	15					20	•				25					
			GTA												_	192
30	THE	nsn	Val	wrq	35	TÀL	GIII	GIH	гλя	40	GTÅ	GIII	Set	FIO	45	

			TCC Ser							240
			GGT Gly							288
			GCC Ala					•	,	<b>33</b> 6
			CAA Gln 100							378
C-										379

#### (2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

#### (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

1 5 10

Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid

()

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

			•								
(xi)	SEQUENCE	DESCRIPTION	ON: SEQ	ID NO	o: 78	:					
CAGAGCCAF	AA AGTTCCT	GAG CGCCA	G	٠							26
(2) INFOR	RMATION FO	R SEQ ID	NO:79:								
(i)	(B) TYPE (C) STRA	CHARACTER TH: 26 ba : nucleic NDEDNESS: LOGY: line	se pairs acid single	1 .							
	•	•									
/ ar i \	SEQUENCE		ON SEC	TD NO				,	,		
	SEQUENCE			ID NO	J. 13.		•				
CTCAGGAAC	CT TTTGGCT	CTG GGTCA	r ′	•							26
(2) INFOR	RMATION FO	R SEQ ID I	:08:0			•					
(i)	(B) TYPE (C) STRA	CHARACTER TH: 379 ba : nucleic NDEDNESS: LOGY: line	ase pair acid double	s		• .		. •	٠.		
	·										•
(ix)	• •	/KEY: CDS TION: 1	378				•				
(ix)		/KEY: mat TION: 58.								-	
(xi)	SEQUENCE	DESCRIPTIO	ON: SEQ	ID NO	80:	:					
	CGG AGC TG Crp Ser Cy -1	s Ile Ile									48
	CCC GAC AT Ser Asp Il										96
	GGT GAC AG Gly Asp Ar										144

			GTA Val														192
			TAC Tyr														240
			AGC Ser 65														288
			GAG Glu														336
			GCG Ala														378
С																•	379
(2)			(B)	NCE LEN TYE	CHAF	,	RIST ami	TICS: Ino a		5	·						
	( i	i) M	OLEC	ULE	TYPE	E: pr	otei	_n									
	( ×	i) S	SEQUE	NCE	DESC	CRIPI	CION:	SEÇ	2 ID	ио: 8	31:						
Met -19	Gly	Trp	Ser	Cys -15	Ile	Ile	Leu	Ser	Leu -10	Val	Ala	Thr	Ala	Thr -5	Gly		
Val	His	Ser	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Gln	Lys	Phe 10	Leu	Ser	Ala		
Ser	Val 15	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Lys	Ala 25	Ser	Gln	Asn	Val		
Gly 30	Thr	Asn	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Gln	Ser	Pro	Lys 45		

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg

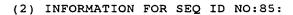
Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105 (2) INFORMATION FOR SEQ ID NO:82:

(i)	(B) TYPE: 1	: 29 base pa nucleic acid EDNESS: sing	irs						
							•		
		•							
(xi)	SEQUENCE DES	SCRIPTION: SI	EQ ID NO	:82:					
GGACAGAG	TC CAAAGCTGCT	GATCTACTC				•			2
(2) INFO	RMATION FOR S	SEQ ID NO:83	:						
		29 base pai nucleic acid CDNESS: singl	irs						
				· ,					
(xi)	SEQUENCE DES	CRIPTION: SE	EQ ID NO	:83:					
ATCAGCAG	CT TTGGACTCT	TCCTGGCTT							29
(2) INFO	RMATION FOR S	EQ ID NO:84:	:						•
(i)	(B) TYPE: n	379 base pa ucleic acid DNESS: doubl	airs						
•									
(ix)	FEATURE: (A) NAME/KE (B) LOCATION							•	
(ix)		Y: mat_pepti N: 58378	lde						
(xi)	SEQUENCE DES	CRIPTION: SE	Q ID NO	:84:					
	TGG AGC TGT A Trp Ser Cys I -15								4.8
	CC GAC ATC C								96
val His S	Ser Asp Ile G	In Met Thr G	in Ser	rro Ser	Ser Leu 10	ser	Ala		

			ACC Thr 20						14
			TAC Tyr						19
			TCC Ser		Ser				24
			GGT Gly						28
			GCC Ala				Tyr		
			CAA Gln 100						378
С									379



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 126 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 30 35 40 45

Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90



Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 (2) INFORMATION FOR SEQ ID NO:86: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..378 (ix) FEATURE: (A) NAME/KEY: mat\_peptide (B) LOCATION: 58..378 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86: 48 ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly \_\_10 -19 -15 96 GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 5 AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144 Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 20 GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192 Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys 35 240 CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 50 55 288 TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

65

80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser

70

379

336

378

- (2) INFORMATION FOR SEQ ID NO:87:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 126 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

1 5 10

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25

Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
30 35 40 45

Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
50 55 60

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90

23

Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105

- (2) INFORMATION FOR SEQ ID NO:88:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 23 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GCTCCAAAGC CGCTGATCTA CTC

- (2) INFORMATION FOR SEQ ID NO:89:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 23 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

TAGATCAGCG GCTTTGGAGC CTT	23
(2) INFORMATION FOR SEQ ID NO:90:	·
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 379 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1378	
<pre>(ix) FEATURE:     (A) NAME/KEY: mat_peptide     (B) LOCATION: 58378</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	÷
ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10 -5	48
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala 1 5 10	96
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val 15 20 25	144
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40 45	192
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 50 55 60	240
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC  Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  65 70 75	288
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90	336

378

379

		CGG Arg													
	95					100			•		105			•	
С															
(2)	INF	ORMA:	rion	FOR	SEQ	ID I	NO: 9	1:							
		(i) s	(A)	LEI TYI	NGTH:	: 126 amino	ERIST 5 am: 5 ac: linea	ino a id		5			•		
	(	ii) 1	MOLE	CULE	TYPE	E: pı	rote	Ĺn					-		
	(:	ki) S	SEQUI	ENCE	DESC	CRIP	rion	SEQ	Q ID	NO:	91:				.*
Met -19	Gly	Trp	Ser	Cys -15	Ile	Ile	Leu	Ser	Leu -10	Val	Ala	Thr	Ala	Thr -5	Gly
Val	His	Ser	Asp 1	Ile	Gln	Met	Thr 5	Gln	Ser	Pro	Ser	Ser 10	Leu	Ser	Ala
Ser	Val 15	Gly	Asp	Arg	Val	Thr 20	Ile	Thr	Cys	Lys	Ala 25	Ser	Gln	Asn	Val
Gly 30	Thr	Asn	Val	Ala	Trp 35	Tyr	Gln	Gln	Lys	Pro 40	Gly	Lys	Ala	Pro	Lys 45
Pro	Leu	Ile	Tyr	Ser 50	Ala	Ser	Tyr	Arg	Tyr 55	Ser	Gly	Val	Pro	Ser 60	Arg
Phe	Ser	Gly	Ser 65	Gly	Ser	Gly	Thr	Asp 70	Phe	Thr	Phe	Thr	Ile 75	Ser	Ser
Leu	Gln	Pro 80	Glu	Asp	Ile	Ala	Thr 85	Tyr	Tyr	CÀa	Gln	Gln 90	Tyr	Asn	Ser
Tyr	Pro 95	Arg	Ala	Phe	Gly	Gln 100		Thr	Lys	Val	Glu 105	Ile	Lys	•	
(2)	INF	ORMA	rion	FOR	SEQ	ID I	NO: 92	2:	•						
	(i)	-	QUENC	ENGTI	i: 13	37 ba	ase p	pair	3		٠				

(D) TOPOLOGY: linear

(C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

AAGAAGCCTG GGTCCTCAGT GAAGGTCTCC TGCAAGGCTT CTGGCTTCAA CATTAAAGAC 60
ACCTATATAC ACTGGGTGCG CCAGGCTCCA GGACAGGGCC TGGAGTGGAT GGGAAGGATT 120



GATCCTGAGG ATGGTAA	137
(2) INFORMATION FOR SEQ ID NO:93:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 111 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
TGAGATCTGA GGACACAGCC TTTTATTTCT GTGCAAGTGC CTACTATGTT AACCAGGACT	60
ACTGGGGCCA AGGGACCACT GTCACCGTCT CCTCAGGTGA GTGGATCCGA C	111
(2) INFORMATION FOR SEQ ID NO:94:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 130 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	•
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:	
ACCTTCACTG AGGACCCAGG CTTCTTCACC TCAGCTCCAG ACTGCACCAG CTGCACCTGG	60
GAGTGAGCAC CTGGAGCTAC AGCCAGCAAG AAGAAGACCC TCCAGGTCCA GTCCATGGTC	120
GAAGCTTATC	130
(2) INFORMATION FOR SEQ ID NO:95:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 132 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
AAAGGCTGTG TCCTCAGATC TCAGGCTGCT GAGCTCCATG TAGGCTGTGT TCGTGGATTC	60
GTCTGCAGTG ATTGTGACTC GGCCCTGGAA CTTCGGGTCA TATTTAGTAT TACCATCCGC	120



		- 89 -			
AGG	ATCAATC CT				132
(2)	INFORMATION FOR SEQ ID NO:96:				
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 25 base pair</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	·s			
	•				
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:96:		•	
GAT	AAGCTTC CACCATGGAC TGGAC				25
(2)	INFORMATION FOR SEQ ID NO:97:				
	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 25 base pair</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	s			
				•	
	(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:97:			
GTC	GGATCCA CTCACCTGAG GAGAC				25
(2)	INFORMATION FOR SEQ ID NO:98:				
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 409 base pai</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>				
	· ·				

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..408
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 58..408
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATG GAC TGG ACC TGG AGG GTC TTC TTC TTG CTG GCT GTA GCT CCA GGT Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly -19 -15 -5

									- 90	-							
	CAC His		Gln				Val					Glu					96
CCT	GGG	TCC	1 TCA	GTG	AAG	GTC	5 TCC	TGC	AAG	GCT	тст	10 GGC	TTC	AAC	ATT		144
Pro	Gly 15	Ser	Ser	Val	Lys	Val 20	Ser	Cys	Lys	Ala	Ser 25	Gly	Phe	Asn	Ile		
	GAC Asp																192
	TGG Trp																240
	AAG Lys																288
	GCC Ala		,												TTT Phe		336
	TTC Phe 95	Cys															384
	ACC Thr		,					G .									409
(2)	INFO	ORMAT	rion	FOR	SEQ	ID. I	10:99	):									
	(	(i) S	(A)	LEN TYP	NGTH:	RACTI : 136 amino GY: 1	ami aci	ino a id		3						·	
	i )	Li) N	OLEC	CULE	TYPE	E: pi	otei	Ln									
	()	(i) S	SEQUE	ENCE	DESC	CRIPT	:NOI	: SEÇ	O ID	NO:9	99:	÷			•		

Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly -10

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile

Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu . 40

Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp

Pro	гÃг	Pne	65 65	GIY.	Arg	vai	THE	70	Int	Ala	Asp	GIU	75	Int	ASII		
Thr	Ala	Tyr 80	Met	Glu	Leu	Ser	Ser 85	Leu	Arg	Ser	Glu	Asp 90	Thr	Ala	Phe		
Tyr	Phe 95	Cys	Ala	Ser	Ala	Tyr 100	_	Val	Asn	Gln	Asp 105	Tyr	Trp	Gly	Gln		
Gly 110	Thr	Thr	Val	Thr	Val 115	Ser	Ser										
(2)	INFO	ORMA	rion	FOR	SEQ	ID i	NO:10	20:									
	(i)	( P ( E	A) LI B) T C) S	CE CHENGTH YPE: TRANI	nucl	l bas Leic ESS:	se pa acio sino	airs d									
			•							•							
	(xi)	SEÇ	OUENC	CE DE	ESCRI	PTIC	ON: S	SEQ 1	ED NO	:100	):						
AGCT	TGTC	CAC C	CGTCT	CCT	CA GO	TGGT	rggto	GTT	rcggo	TGG	TGGT	GGT1	rcg (	GTGC	STGGCG		60
GATO	CGGAC	AT C	CCAG	ATGAC	CC CF	AGG									•		84
(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	10:10	01:									
	(i)	( <i>P</i> (E	A) LE B) TY C) S7	CE CHENGTH PE: TRANE	i: 84 nucl	bas eic SS:	se pa acio sino	airs 1									
	(xi)	SEÇ	QUENC	CE DE	SCRI	PTIC	on: . s	SEQ 1	D NO	p: 101	L:					. •	
AATI	CCTG	GG C	CATO	CTGGA	T GI	CCGF	ATCC	G CCI	ACCAC	CCG	AACC	CACCE	ACC F	ACCCC	GAACCA		60
CCAC	CACC	TG A	AGGAC	ACGO	T GA	CA											84
(2)	INFO	RMAI	NOI	FOR	SEQ	ID N	10:10	02:									
	(i)	( A ( E	A) LE B) TY C) ST	CE CHENGTH PE: TRAND	i: 34 nucl	bas eic SS:	se pa acio sino	airs 1									

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:	•
CAGCCATGGC GCAGTGTGCA GCTGGTGCAG TCTG	34
(2) INFORMATION FOR SEQ ID NO:103:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 41 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:	
CCACCGAAC CACCACCA TGAGGAGACG GTGACAGTGG T	41
(2) INFORMATION FOR SEQ ID NO:104:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 41 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
GGGACCACTG TCACCGTCTC CTCAGGTGGT GGTGGTTCGG G	41
(2) INFORMATION FOR SEQ ID NO:105:	•
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 41 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	
(D) TOPOLOGY: linear	*
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:	
GGGCTCTGGG TCATCTGGAT GTCCGATCCG CCACCACCCG A	41
(2) INFORMATION FOR SEQ ID NO:106:	
<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 44 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	

## (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:	
TCGGACATCC AGATGACCCA GAGCCCAAGC AGCCTGAGCG CCAG	44
(2) INFORMATION FOR SEQ ID NO:107:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 57 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:	
CAAGAATTCT TATTATTTAT CGTCATCGTC TTTGTAGTCT TTGATTTCGA CCTTGGT	57
(2) INFORMATION FOR SEQ ID NO:108:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 822 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: double</li> <li>(D) TOPOLOGY: linear</li> </ul>	ć
(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1807	
<pre>(ix) FEATURE:    (A) NAME/KEY: mat_peptide    (B) LOCATION: 1807</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:	
ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC GCT Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala 1 5 10	4.8
GCC CAA CCA GCC ATG GCG CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu 20 25 30	96
GTG AAG AAG CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC  Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly  35  40  45	L <b>4</b> 4

				TAT Tyr 55			_	_		_		192
				GGA Gly								240
				CAG Gln								288
				ATG Met								336
				GCA Ala	Ala							384
				GTC Val 135		Ser						432
				GGT Gly								480
				GCC Ala								528
				GTG Val							-	576
				AAG Lys				-				624
				AGA Arg 215						GAC Asp		672
				AGC Ser								720
				AGC Ser								768
				TAC Tyr				TAAT	AAG	AAT		817
тстт	'G							٠				822

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#### (2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 269 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met Lys Tyr Leu Leu Pro Thr Ala Ala Gly Leu Leu Leu Ala 1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu 20 25 30

Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly 35 40 45

Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly 50 55 60

Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr
65 70 75 80

Lys Tyr Asp Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu 85 90 95

Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp 100 105 110

Thr Ala Phe Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr 115 120 125

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser 130 135 140

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln 145 150 155 160

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr 165 170 175

Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln 180 185 190

Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg 195 200 205

Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp 210 215 220

Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr 225 230 235 240

Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg Ala Phe Gly Gln Gly Thr 245 250 255



Lys Val Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys 260 265

- (2) INFORMATION FOR SEQ ID NO:110:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 45 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..45
  - (ix) FEATURE:
    - (A) NAME/KEY: mat\_peptide
    - (B) LOCATION: 1..45
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGT GGT GGT TCG GGT GGT GGT GGT TCG GGT GGC GGA TCG
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

45

- (2) INFORMATION FOR SEQ ID NO:111:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:112:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 87 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Trp Tyr Gln Gln Lys Pro Gly Lys Ala 20 25 30

Pro Lys Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro 35 40 45

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile 50 55 60

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Phe Gly Gln 65 70 75 80

Gly Thr Lys Val Glu Ile Lys 85

### (2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 76 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Trp Val

Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Arg Val Thr Ile 35 40 45

Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu 50 55 60

Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys Ala Gly 65 70 75

#### (2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO:115:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Asp Thr Tyr Ile His
1 5

- (2) INFORMATION FOR SEQ ID NO:116:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 17 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp Pro Lys Phe Gln
1 10 15

Gly

- (2) INFORMATION FOR SEQ ID NO:117:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 8 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Tyr Tyr Val Asn Gln Asp Tyr



- (2) INFORMATION FOR SEQ ID NO:118:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 11 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala 1 5 10

- (2) INFORMATION FOR SEQ ID NO:119:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 7 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Ser Ala Ser Tyr Arg Tyr Ser 1 5

- (2) INFORMATION FOR SEQ ID NO:120:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Gln Gln Tyr Asn Ser Tyr Pro Arg Ala

- (2) INFORMATION FOR SEQ ID'NO:121:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 23 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear

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	ii	MOLECULE	TYPE:	proteir
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/vil	SPOURNCE	DESCRIPTION:	SEC	TD	NO-121.
(XI)	SECUENCE	DESCRIPTION:	350	T D	MO:IZI:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys 20

### (2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys
20 25 30

## (2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

- (2) INFORMATION FOR SEQ ID NO:125:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile Tyr 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:126:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys 20 25 30

- (2) INFORMATION FOR SEQ ID NO:127:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 14 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly 1 5 10

- (2) INFORMATION FOR SEQ ID NO:128:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 32 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

. Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys Ala Ser 20 25 30

- (2) INFORMATION FOR SEQ ID NO:129:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 11 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser 1 5 10

- (2) INFORMATION FOR SEQ ID NO:130:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 107 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: protein
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn 20 25

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile 35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly 50 55

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg 85 90 95

Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

# (2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
10 15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn 20 25

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Pro Leu Ile 35 40 45

Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly 50 60

Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro
65 75 80

Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg 85

Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 100 105

# (2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

#### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile Lys Asp Thr 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met 35 40 45

Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp Pro Lys Phe 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn Thr Ala Tyr 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe Tyr Phe Cys 85 90 95

Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln Gly Thr Thr 100 105 110

Val Thr Val Ser Ser 115

B